

SEQUENCE LISTING

<110> SUNTORY LIMITED

<120> Gene encoding for proteins regulating the pH of vacuoles

<130> 994020

<160> 20

<210> 1

<211> 2237

<212> DNA

<213> Ipomea nil

<223> Nucleotide sequence of DNA encoding for protein regulating the pH of vacuoles

<400> 1

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tcttcatcct tcaacactac cccacatct cacctttcaa gtgatttgta tgttttcggg    180
agggattgga atgggcaacc cggatatgtg aacagaaacc acgacattgg gaaaagattt    240
attgcaaaaa ttgttttgat tgttttggat tttgtggtag aaaaagggga agaacaaaa    299
atg gcg ttc ggg ttg tct tct ttg ctc caa aat tcg gat ttg ttc acg    347
Met Ala Phe Gly Leu Ser Ser Leu Leu Gln Asn Ser Asp Leu Phe Thr
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tct gat cat gct tcc gtt gtg tcg atg aac ctc ttt gtg gcg ttg ctt    395
Ser Asp His Ala Ser Val Val Ser Met Asn Leu Phe Val Ala Leu Leu
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tgc gca tgc att gtt ctt ggc cat cta ctc gag gag aat cgc tgg gtg    443
Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val
      35              40              45

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50 55 60	
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Ile Leu Leu Leu Ser Gly Gly Lys Ser Ser His Leu Leu Val Phe Ser	
65 70 75 80	
gaa gat ctt ttc ttt ata tat ctc ctg cca cct ata ata ttc aat gcg	587
Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala	
85 90 95	
ggg ttt caa gtg aaa aag aag cag ttt ttc gtg aac ttc atg aca att	635
Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Val Asn Phe Met Thr Ile	
100 105 110	
atg ctg ttt gga gct att ggc aca ctt att agc tgt tct att ata tca	683
Met Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Cys Ser Ile Ile Ser	
115 120 125	
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Phe Gly Ala Val Lys Ile Phe Lys His Leu Asp Ile Asp Phe Leu Asp	
130 135 140	
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Phe Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser	
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Val Cys Thr Leu Gln Val Leu Ser Gln Asp Glu Thr Pro Leu Leu Tyr	
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Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val	
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Leu Phe Asn Ala Ile Gln Ser Phe Asp Met Thr Ser Phe Asp Pro Lys	
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Thr Phe Leu Gly Val Gly Ile Gly Leu Leu Cys Ala Tyr Ile Ile Lys	
225 230 235 240	

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Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met	
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Met Leu Met Ser Tyr Leu Ser Tyr Ile Met Ala Glu Leu Phe Tyr Leu	
260 265 270	
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Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr	
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Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Arg His Ser	
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Phe Ala Thr Leu Ser Phe Val Ala Glu Thr Phe Ile Phe Leu Tyr Val	
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Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Lys Asn Ser	
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Gln Gly Leu Ser Val Ala Val Ser Ser Ile Leu Val Gly Leu Ile Leu	
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Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu	
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Ala Lys Lys Asn Ser Ser Asp Lys Ile Ser Phe Arg Gln Gln Ile Ile	
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Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala	
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Tyr Asn Lys Phe Thr Thr Ser Gly His Thr Ser Leu His Glu Asn Ala	
405 410 415	
ata atg att aca agt act gtt acg gtt gtt ctg ttc agc aca gtt gta	1595
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420 425 430	

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aag cag atg cca agc ggt cat tcg tca atg aca aca tcc gaa ccc agt 1691
Lys Gln Met Pro Ser Gly His Ser Ser Met Thr Thr Ser Glu Pro Ser
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agt ccg aag cac ttc acg gtg cca ctc ctg gac aac caa cct gac tca 1739
Ser Pro Lys His Phe Thr Val Pro Leu Leu Asp Asn Gln Pro Asp Ser
465              470              475              480

gaa agc gat atg ata acc gga cct gag gtt gct cga cca act gcc ttg 1787
Glu Ser Asp Met Ile Thr Gly Pro Glu Val Ala Arg Pro Thr Ala Leu
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cgc atg ctg cta agg acg cca acc cac acc gtg cac cgc tac tgg cgt 1835
Arg Met Leu Leu Arg Thr Pro Thr His Thr Val His Arg Tyr Trp Arg
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Lys Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe
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gtt ccg ttt gtc gcg ggc tca cca gtt gag cag agc cct aga tga 1928
Val Pro Phe Val Ala Gly Ser Pro Val Glu Gln Ser Pro Arg
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<213> Ipomea nil

<223> Amino acid sequence of protein regulating the pH
of vacuoles

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Cys	Ala	Cys	Ile	Val	Leu	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg	Trp	Val
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Asn	Glu	Ser	Ile	Thr	Ala	Leu	Ile	Ile	Gly	Leu	Cys	Thr	Gly	Val	Val
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Ile	Leu	Leu	Leu	Ser	Gly	Gly	Lys	Ser	Ser	His	Leu	Leu	Val	Phe	Ser
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Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn	Ala
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Gly	Phe	Gln	Val	Lys	Lys	Lys	Gln	Phe	Phe	Val	Asn	Phe	Met	Thr	Ile
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Phe	Gly	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp	Ser
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Val	Cys	Thr	Leu	Gln	Val	Leu	Ser	Gln	Asp	Glu	Thr	Pro	Leu	Leu	Tyr
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Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val
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Thr	Phe	Leu	Gly	Val	Gly	Ile	Gly	Leu	Leu	Cys	Ala	Tyr	Ile	Ile	Lys
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Lys	Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Leu	Met
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Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser	His	Tyr			
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Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Val	Thr	Thr	Arg	His	Ser			
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Lys	Gln	Met	Pro	Ser	Gly	His	Ser	Ser	Met	Thr	Thr	Ser	Glu	Pro	Ser			
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Arg	Met	Leu	Leu	Arg	Thr	Pro	Thr	His	Thr	Val	His	Arg	Tyr	Trp	Arg			
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Lys	Phe	Asp	Asp	Ser	Phe	Met	Arg	Pro	Val	Phe	Gly	Gly	Arg	Gly	Phe			
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<223> MseI adaptor

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16

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<223> MseI+N primer

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22

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22

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 <213> Petunia hybrida

<223> Nucleotide sequence of DNA encoding for protein
 regulating the pH of vacuoles

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gtggtgtttt aagctcaatt cgacgtcgtt tttactggaa ttctgatcag taaatagggc 240
tattttgatg taaggttgtg aaagtttaca gtttggaagt tgagtttagtg aaaaagggga 300
aactttattg tgatattttc acaagtattt ggtgaattca ggttattgag a atg gct 357
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ttt gat ttt ggg acg ttg ttg gga aat gta gac agg tta tcg aca tct 405
Phe Asp Phe Gly Thr Leu Leu Gly Asn Val Asp Arg Leu Ser Thr Ser
      5              10              15
gat cat caa tca gtt gtg tcg ata aac tta ttc gtt gct ctt att tgc 453
Asp His Gln Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Ile Cys
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gcg tgt att gtg atc ggt cat ttg ttg gaa gaa aac aga tgg atg aat 501
Ala Cys Ile Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn
      35              40              45              50
gag tcc ata act gcc tta gtg att ggt tct tgt act gga atc gtt att 549
Glu Ser Ile Thr Ala Leu Val Ile Gly Ser Cys Thr Gly Ile Val Ile
      55              60              65
cta ctg ata agt gga gga aag aac tct cat att tta gtg ttc agt gaa 597
Leu Leu Ile Ser Gly Gly Lys Asn Ser His Ile Leu Val Phe Ser Glu
      70              75              80
gat ctt ttc ttc att tac ctt ctt ccg cca atc att ttt aat gct ggg 645
Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly
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Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Leu	
	180					185					190					
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Phe	Asn	Ala	Ile	Gln	Asn	Phe	Asp	Leu	Ser	His	Ile	Asp	Thr	Gly	Lys	
	195				200					205					210	
gct	atg	gaa	tta	gtt	gga	aac	ttt	cta	tac	ttg	ttt	gcc	tca	agc	act	1029
Ala	Met	Glu	Leu	Val	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Ala	Ser	Ser	Thr	
				215					220				225			
gcc	cta	gga	gtt	gct	gct	ggc	cta	ctg	agc	gcc	tat	att	att	aaa	aaa	1077
Ala	Leu	Gly	Val	Ala	Ala	Gly	Leu	Leu	Ser	Ala	Tyr	Ile	Ile	Lys	Lys	
			230					235					240			
ctc	tac	ttt	gga	agg	cac	tca	act	gac	cgt	gag	gtt	gct	ata	atg	ata	1125
Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Ile	Met	Ile	
		245					250					255				
ctc	atg	gct	tac	cta	tct	tac	atg	ctt	gct	gaa	tta	ttc	tat	tta	agt	1173
Leu	Met	Ala	Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe	Tyr	Leu	Ser	
	260					265					270					

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Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Thr Phe	
295 300 305	
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Ala Thr Leu Ser Phe Ile Ala Glu Ile Phe Ile Phe Leu Tyr Val Gly	
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Gly Ile Ser Val Gln Val Ser Ser Ile Leu Leu Gly Leu Val Leu Val	
340 345 350	
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Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Thr	
355 360 365 370	
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Lys Lys Thr Pro Glu Ala Lys Ile Ser Phe Asn Gln Gln Val Thr Ile	
375 380 385	
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Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr	
390 395 400	
aat cag ttt acc agg gga ggt cat act cag tta cgc gca aat gca ata	1605
Asn Gln Phe Thr Arg Gly Gly His Thr Gln Leu Arg Ala Asn Ala Ile	
405 410 415	
atg atc aca agt act atc act gtt gtc ctt ttc agc aca gtc gtg ttt	1653
Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Val Val Phe	
420 425 430	
ggg ttg atg aca aaa cct ttg att aga ata ttg cta ccc tca cac aaa	1701
Gly Leu Met Thr Lys Pro Leu Ile Arg Ile Leu Leu Pro Ser His Lys	
435 440 445 450	
cac ttg agc aga atg atc tct tct gaa cca acg acc cca aaa tcc ttc	1749
His Leu Ser Arg Met Ile Ser Ser Glu Pro Thr Thr Pro Lys Ser Phe	
455 460 465	

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cgc cat gta ccc cgt ccc cac agt ttg cgg atg ctc ctt tca acc cca 1845
Arg His Val Pro Arg Pro His Ser Leu Arg Met Leu Leu Ser Thr Pro
          485                      490                      495
tct cat aca gtg cat tat tac tgg aga aag ttt gac aat gca ttc atg 1893
Ser His Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asn Ala Phe Met
          500                      505                      510
cgt cca gtt ttc ggt gga cga ggt ttt gta cct ttt gct cca gga tca 1941
Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Ala Pro Gly Ser
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ccg aca gac cca gtt ggt gga aat ttg caa tgatggagat acagattgca 1991
Pro Thr Asp Pro Val Gly Gly Asn Leu Gln
          535                      540
aaaagtggtc ttggtgaggg aagagggcag ttttttggtgta atgaggttcc gttttcttta 2051
atgttaatag caagtgtggt taaaaagggg ttgtctagtt tataggtttt gcagatctca 2111
agtatatattca tttgggtgat catgtttttca gctcagttat tgcttttggt cattgctgac 2171
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tttgcaattt atcgaaacac caaatgggtg tatattctgt aagcttgtgg catagctagc 2291
ttaattgtct tgtaaaattt cctacaggtt agagattggt tcttgatatg tagatttcat 2351
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<210> 15

<211> 540

<212> PRT

<213> Petunia hybrida

<223> Amino acid sequence of protein regulating the pH
of vacuoles

<400> 15

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Val	Gly	Met	Asp	Ala	Leu	Asp	Ile	Glu	Lys	Trp	Lys	Phe	Val	Ser	Asp	325	330	335	
Ser	Pro	Gly	Ile	Ser	Val	Gln	Val	Ser	Ser	Ile	Leu	Leu	Gly	Leu	Val	340	345	350	
Leu	Val	Gly	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	355	360	365	
Leu	Thr	Lys	Lys	Thr	Pro	Glu	Ala	Lys	Ile	Ser	Phe	Asn	Gln	Gln	Val	370	375	380	
Thr	Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu	385	390	395	400
Ala	Tyr	Asn	Gln	Phe	Thr	Arg	Gly	Gly	His	Thr	Gln	Leu	Arg	Ala	Asn	405	410	415	
Ala	Ile	Met	Ile	Thr	Ser	Thr	Ile	Thr	Val	Val	Leu	Phe	Ser	Thr	Val	420	425	430	
Val	Phe	Gly	Leu	Met	Thr	Lys	Pro	Leu	Ile	Arg	Ile	Leu	Leu	Pro	Ser	435	440	445	
His	Lys	His	Leu	Ser	Arg	Met	Ile	Ser	Ser	Glu	Pro	Thr	Thr	Pro	Lys	450	455	460	
Ser	Phe	Ile	Val	Pro	Leu	Leu	Asp	Ser	Thr	Gln	Asp	Ser	Glu	Ala	Asp	465	470	475	480
Leu	Glu	Arg	His	Val	Pro	Arg	Pro	His	Ser	Leu	Arg	Met	Leu	Leu	Ser	485	490	495	
Thr	Pro	Ser	His	Thr	Val	His	Tyr	Tyr	Trp	Arg	Lys	Phe	Asp	Asn	Ala	500	505	510	
Phe	Met	Arg	Pro	Val	Phe	Gly	Gly	Arg	Gly	Phe	Val	Pro	Phe	Ala	Pro	515	520	525	
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<210> 16
 <211> 2553
 <212> DNA

<213> Nierembergia hybrida

<223> Nucleotide sequence of DNA encoding for protein
regulating the pH of vacuoles

<400> 16

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tcgtcttctc aatctgcttt caaatccttt ttgtttgtga tattcgatat tattcactca 180
gtttacctta atatttcctc gcactttctg aattcgagtg ctttgaagtg tgttggattt 240
cgaaaagcgg aagaaaattc agcaaaaacg ctgttgctga atttgcagca gtttgagttt 300
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cgttttgact gcaatatttg tccgtgattc ggactttgtt gaaattttgc tatttgaaat 420
ttgaatgtaa ggttgtcata gctttgccac tcggaaatac agtcagtgag aaagaaaaaa 480
aactgtgtag tgttttttcc acaagtattt ggtgaattga ggttcttgaa atg gcg 536
                                     Met Ala
ttt gac ttt ggg act ctg ctg gga aag atg aac aac tta aca act tct 584
Phe Asp Phe Gly Thr Leu Leu Gly Lys Met Asn Asn Leu Thr Thr Ser
      5              10              15
gat cat caa tca gtg gtg tcg gta aac ttg ttt gtt gca ctt att tgc 632
Asp His Gln Ser Val Val Ser Val Asn Leu Phe Val Ala Leu Ile Cys
      20              25              30
gcg tgt att gtg atc ggt cat tta ttg gag gaa aac aga tgg atg aat 680
Ala Cys Ile Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn
      35              40              45              50
gag tcc ata act gcc ctt gtg att ggt agt tgc act gga gtc atc att 728
Glu Ser Ile Thr Ala Leu Val Ile Gly Ser Cys Thr Gly Val Ile Ile
      55              60              65
cta cta ata agt gga gga aag aac tca cat att tta gtg ttc agc gaa 776
Leu Leu Ile Ser Gly Gly Lys Asn Ser His Ile Leu Val Phe Ser Glu
      70              75              80
gat ctt ttc ttc att tac ctt ctt cca ccg atc att ttt aat gct ggg 824
Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly
      85              90              95
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Leu	Phe	Gly	Ala	Val	Gly	Thr	Leu	Ile	Ser	Phe	Ile	Ile	Ile	Ser	Ala	
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Gly	Ala	Ile	Gly	Ile	Phe	Lys	Lys	Met	Asp	Ile	Gly	His	Leu	Glu	Ile	
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gga	gat	tac	ctt	gca	att	gga	gca	atc	ttt	gct	gca	aca	gat	tct	gta	1016
Gly	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp	Ser	Val	
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tgc	acc	tta	caa	gtg	ctt	aat	cag	gaa	gaa	aca	ccg	tta	ttg	tac	agt	1064
Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Glu	Glu	Thr	Pro	Leu	Leu	Tyr	Ser	
		165					170					175				
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Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Leu	
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Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Ile	Met	Ile	
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Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Val	Thr	Thr	Lys	His	Thr	Phe	
			295						300					305		
gct	aca	tta	tca	ttt	att	gct	gaa	ata	ttc	ata	ttc	ctt	tat	gtt	ggt	1496
Ala	Thr	Leu	Ser	Phe	Ile	Ala	Glu	Ile	Phe	Ile	Phe	Leu	Tyr	Val	Gly	
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Met	Asp	Ala	Leu	Asp	Ile	Glu	Lys	Trp	Lys	Phe	Val	Ser	Asp	Ser	Pro	
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gga	agg	gga	gcc	ttt	gtt	ttc	ccc	ttg	tca	ttc	ttg	tcc	aac	ttg	acc	1640
Gly	Arg	Gly	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	Leu	Thr	
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Lys	Lys	Asn	Pro	Glu	Asp	Lys	Ile	Ser	Phe	Asn	Gln	Gln	Val	Thr	Ile	
			375					380					385			
tgg	tgg	gct	ggg	ctt	atg	cga	ggt	gct	gtt	tct	atg	gcc	ctt	gct	tat	1736
Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu	Ala	Tyr	
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Asn	Gln	Phe	Thr	Arg	Gly	Gly	His	Thr	Gln	Leu	Arg	Ala	Asn	Ala	Ile	
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His	Leu	Ile	Arg	Met	Ile	Ser	Ser	Glu	Pro	Met	Thr	Pro	Lys	Ser	Phe	
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att	gtg	cca	ctt	ctt	gac	agc	aca	caa	gac	tca	gaa	gct	gat	ctg	ggc	1976
Ile	Val	Pro	Leu	Leu	Asp	Ser	Thr	Gln	Asp	Ser	Glu	Ala	Asp	Leu	Gly	
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 Arg His Val Pro Arg Pro His Ser Leu Arg Met Leu Leu Ser Thr Pro
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 tct cac acg gta cat tac tac tgg aga aaa ttt gac aat gca ttc atg 2072
 Ser His Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asn Ala Phe Met
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 cgt cct gtt ttc ggt gga cga ggt ttt gta cct ttt gtt cca gga tca 2120
 Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser
 515 520 525 530
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 Pro Thr Glu Pro Val Glu Pro Thr Glu Pro Arg Pro Ala Glu Ser Arg
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 cca acc gaa cca act gat gag tgattacact gatggagatg caggttgac 2219
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<210> 17

<211> 553

<212> PRT

<213> Nierembergia hybrida

<223> Amino acid sequence of protein regulating the pH
of vacuoles

<400> 17

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	35						40					45			
Met	Asn	Glu	Ser	Ile	Thr	Ala	Leu	Val	Ile	Gly	Ser	Cys	Thr	Gly	Val
	50						55					60			
Ile	Ile	Leu	Leu	Ile	Ser	Gly	Gly	Lys	Asn	Ser	His	Ile	Leu	Val	Phe
65					70					75					80
Ser	Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Ile	Phe	Asn
				85					90					95	
Ala	Gly	Phe	Gln	Val	Lys	Lys	Lys	Ser	Phe	Phe	Arg	Asn	Phe	Ser	Thr
			100					105					110		
Ile	Met	Leu	Phe	Gly	Ala	Val	Gly	Thr	Leu	Ile	Ser	Phe	Ile	Ile	Ile
	115						120						125		
Ser	Ala	Gly	Ala	Ile	Gly	Ile	Phe	Lys	Lys	Met	Asp	Ile	Gly	His	Leu
	130					135					140				
Glu	Ile	Gly	Asp	Tyr	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp
145					150					155					160
Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Glu	Glu	Thr	Pro	Leu	Leu
				165					170					175	
Tyr	Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val
			180					185					190		
Val	Leu	Phe	Asn	Ala	Val	Gln	Asn	Phe	Asp	Leu	Ser	His	Ile	Ser	Thr
	195						200						205		
Gly	Lys	Ala	Leu	Gln	Leu	Ile	Gly	Asn	Phe	Leu	Tyr	Leu	Phe	Ala	Ser
	210					215					220				
Ser	Thr	Phe	Leu	Gly	Val	Ala	Val	Gly	Leu	Leu	Ser	Ala	Phe	Ile	Ile
225					230					235					240
Lys	Lys	Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Ile
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		260						265					270		
Leu	Ser	Gly	Ile	Leu	Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser	His
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Tyr	Thr	Trp	His	Asn	Val	Thr	Glu	Ser	Ser	Arg	Val	Thr	Thr	Lys	His
	290					295									300

Thr Phe Ala Thr Leu Ser Phe Ile Ala Glu Ile Phe Ile Phe Leu Tyr
 305 310 315 320
 Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Ser Asp
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 Ser Pro Gly Thr Ser Ile Lys Val Ser Ser Ile Leu Leu Gly Leu Val
 340 345 350
 Leu Val Gly Arg Gly Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn
 355 360 365
 Leu Thr Lys Lys Asn Pro Glu Asp Lys Ile Ser Phe Asn Gln Gln Val
 370 375 380

Thr Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu
 385 390 395 400
 Ala Tyr Asn Gln Phe Thr Arg Gly Gly His Thr Gln Leu Arg Ala Asn
 405 410 415
 Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Val
 420 425 430
 Val Phe Gly Leu Met Thr Lys Pro Leu Ile Leu Leu Leu Leu Pro Ser
 435 440 445
 Gln Lys His Leu Ile Arg Met Ile Ser Ser Glu Pro Met Thr Pro Lys
 450 455 460
 Ser Phe Ile Val Pro Leu Leu Asp Ser Thr Gln Asp Ser Glu Ala Asp
 465 470 475 480
 Leu Gly Arg His Val Pro Arg Pro His Ser Leu Arg Met Leu Leu Ser
 485 490 495
 Thr Pro Ser His Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asn Ala
 500 505 510
 Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro
 515 520 525
 Gly Ser Pro Thr Glu Pro Val Glu Pro Thr Glu Pro Arg Pro Ala Glu
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 Ser Arg Pro Thr Glu Pro Thr Asp Glu
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<210> 18
 <211> 2361

<212> DNA

<213> Torenia hybrida

<223> Nucleotide sequence of DNA encoding for protein
regulating the pH of vacuoles

<400> 18

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agcaggagtt tcaactttga gcccgtttat atttataaac aaattccgag tccaaagatt 360
gaactttgaa ataatcaa atcaagcaa gcaat atg ggg ttt gaa tct gta 413

Met Gly Phe Glu Ser Val

5

att aag cta gcg gca agt gaa act gac aat ttg tgg agc tct ggt cac 461
Ile Lys Leu Ala Ala Ser Glu Thr Asp Asn Leu Trp Ser Ser Gly His

10

15

20

ggg tca gtg gtc gct ata acc tta ttt gtc act ctt ctc tgc aca tgt 509
Gly Ser Val Val Ala Ile Thr Leu Phe Val Thr Leu Leu Cys Thr Cys

25

30

35

ata gtg att ggt cat ctt ctg gag gaa aac cgt tgg atg aat gaa tct 557
Ile Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn Glu Ser

40

45

50

atc att gcc ctc ata att ggt tta gcc acg gga gtt ata atc ctg tta 605
Ile Ile Ala Leu Ile Ile Gly Leu Ala Thr Gly Val Ile Ile Leu Leu

55

60

65

70

ata agt ggt gga aaa agc tcc cat ctc ttg gtg ttc agt gag gat ctt 653
Ile Ser Gly Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp Leu

75

80

85

ttc ttc atc tat gcg ctg cca cca atc att ttt aat gcg ggg ttc caa 701
Phe Phe Ile Tyr Ala Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe Gln

90

95

100

gta	aaa	aag	aaa	tca	ttc	ttt	cgc	aat	ttc	gca	act	ata	atg	atg	ttt	749
Val	Lys	Lys	Lys	Ser	Phe	Phe	Arg	Asn	Phe	Ala	Thr	Ile	Met	Met	Phe	
	105						110					115				
gga	gca	gtt	ggt	acc	ttg	ata	tcc	ttc	atc	atc	att	tca	ctc	ggt	aca	797
Gly	Ala	Val	Gly	Thr	Leu	Ile	Ser	Phe	Ile	Ile	Ile	Ser	Leu	Gly	Thr	
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att	gca	ttc	ttc	ccc	aaa	atg	aac	atg	aga	ctt	gga	gtt	gga	gat	tat	845
Ile	Ala	Phe	Phe	Pro	Lys	Met	Asn	Met	Arg	Leu	Gly	Val	Gly	Asp	Tyr	
	135				140					145					150	
ctt	gct	att	gga	gct	att	ttt	gct	gca	aca	gac	tca	gtt	tgc	aca	tta	893
Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ala	Ala	Thr	Asp	Ser	Val	Cys	Thr	Leu	
				155					160					165		
cag	gtg	cta	agc	cag	gac	gaa	aca	cca	ctg	ttg	tac	agt	cta	gtg	ttt	941
Gln	Val	Leu	Ser	Gln	Asp	Glu	Thr	Pro	Leu	Leu	Tyr	Ser	Leu	Val	Phe	
				170				175					180			
ggc	gag	ggt	gtt	gta	aat	gac	gcg	act	tca	gtg	gtc	cta	ttt	aat	gca	989
Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Val	Val	Leu	Phe	Asn	Ala	
		185					190					195				
gta	cag	aac	ttc	gac	ctg	cct	cat	atg	tct	act	gct	aaa	gct	ttc	gag	1037
Val	Gln	Asn	Phe	Asp	Leu	Pro	His	Met	Ser	Thr	Ala	Lys	Ala	Phe	Glu	
	200					205					210					
ctt	gtt	gga	aac	ttc	ttt	tat	tta	ttt	gct	aca	agc	act	gtg	ctg	ggt	1085
Leu	Val	Gly	Asn	Phe	Phe	Tyr	Leu	Phe	Ala	Thr	Ser	Thr	Val	Leu	Gly	
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Val	Leu	Thr	Gly	Leu	Leu	Ser	Ala	Tyr	Ile	Ile	Lys	Lys	Leu	Tyr	Phe	
				235					240					245		
gga	agg	cac	tcc	act	gat	cgc	gag	gtt	gcc	ata	atg	ata	ctc	atg	gct	1181
Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Ile	Met	Ile	Leu	Met	Ala	
			250					255					260			
tat	ctg	tcg	tat	atg	tta	gct	gaa	tta	ttc	gat	ttg	agc	ggt	atc	ctc	1229
Tyr	Leu	Ser	Tyr	Met	Leu	Ala	Glu	Leu	Phe	Asp	Leu	Ser	Gly	Ile	Leu	
	265					270						275				
acc	gtg	ttc	ttc	tgt	gga	att	gtg	atg	tcg	cac	tat	aca	tgg	cac	aat	1277
Thr	Val	Phe	Phe	Cys	Gly	Ile	Val	Met	Ser	His	Tyr	Thr	Trp	His	Asn	
	280					285					290					

gtc act gaa aac tca aga gtt acc acc aag cat aca ttt gcg aca ttg	1325
Val Thr Glu Asn Ser Arg Val Thr Thr Lys His Thr Phe Ala Thr Leu	
295 300 305 310	
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Ser Phe Val Ala Glu Ile Phe Ile Phe Leu Tyr Val Gly Met Asp Ala	
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Leu Asp Ile Glu Lys Trp Arg Phe Val Ser Gly Ser Met Thr Thr Ser	
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gca gct gtc agt gca act ctg ctg gga ttg gtt ttg ctc tca aga gca	1469
Ala Ala Val Ser Ala Thr Leu Leu Gly Leu Val Leu Leu Ser Arg Ala	
345 350 355	
gcc ttt gta ttc cct tta tca ttt ctc tcc aat ctg gcc aaa aag tcc	1517
Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys Lys Ser	
360 365 370	
cca ctc gaa aaa atc agt ctc agg cag caa att ata ata tgg tgg gct	1565
Pro Leu Glu Lys Ile Ser Leu Arg Gln Gln Ile Ile Ile Trp Trp Ala	
375 380 385 390	
ggg ctt atg cgc gga gcc gtt tcc atg gct ctt gct tac aag cag ttt	1613
Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Lys Gln Phe	
395 400 405	
act aga gaa ggt ctc aca gtg gaa cgt gaa aat gcc ata ttc atc acc	1661
Thr Arg Glu Gly Leu Thr Val Glu Arg Glu Asn Ala Ile Phe Ile Thr	
410 415 420	
agt aca atc acc att gtg ctc ttc agc act gtg gtg ttt ggt ttg atg	1709
Ser Thr Ile Thr Ile Val Leu Phe Ser Thr Val Val Phe Gly Leu Met	
425 430 435	
acg aag ccc ctc atc aat tta ctg ata ccc tca cca aag ctt aac aga	1757
Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro Ser Pro Lys Leu Asn Arg	
440 445 450	
tcg gtc tct tca gaa ccg ctg act cca aac tcc atc aca atc cca ctt	1805
Ser Val Ser Ser Glu Pro Leu Thr Pro Asn Ser Ile Thr Ile Pro Leu	
455 460 465 470	
ctc ggg gaa agt cag gac tct gtg gcc gaa cta ttc agc atc aga ggt	1853
Leu Gly Glu Ser Gln Asp Ser Val Ala Glu Leu Phe Ser Ile Arg Gly	
475 480 485	

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490

495

500

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505

510

515

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Phe Asp Asn Ala Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val

520

525

530

cca tat gtt ccc ggt tca ccg act gaa cga agc gtt cgc aac tgg gaa 2045
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535

540

545

550

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Glu Glu Thr Lys Gln

555

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<211> 555

<212> PRT

<213> Torenia hybrida

<223> Amino acid sequence of protein regulating the pH
of vacuoles

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15

Leu Trp Ser Ser Gly His Gly Ser Val Val Ala Ile Thr Leu Phe Val

20

25

30

Thr Leu Leu Cys Thr Cys Ile Val Ile Gly His Leu Leu Glu Glu Asn

35

40

45

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			340					345					350					
Val	Leu	Leu	Ser	Arg	Ala	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser			
		355					360					365						
Asn	Leu	Ala	Lys	Lys	Ser	Pro	Leu	Glu	Lys	Ile	Ser	Leu	Arg	Gln	Gln			
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Ile	Ile	Ile	Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala			
385					390					395					400			
Leu	Ala	Tyr	Lys	Gln	Phe	Thr	Arg	Glu	Gly	Leu	Thr	Val	Glu	Arg	Glu			
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			420					425					430					
Val	Val	Phe	Gly	Leu	Met	Thr	Lys	Pro	Leu	Ile	Asn	Leu	Leu	Ile	Pro			
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Ser	Pro	Lys	Leu	Asn	Arg	Ser	Val	Ser	Ser	Glu	Pro	Leu	Thr	Pro	Asn			
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Ser	Ile	Thr	Ile	Pro	Leu	Leu	Gly	Glu	Ser	Gln	Asp	Ser	Val	Ala	Glu			
465					470					475					480			
Leu	Phe	Ser	Ile	Arg	Gly	Gln	Thr	Ser	Gln	Gly	Gly	Glu	Pro	Val	Ala			
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Arg	Pro	Ser	Ser	Leu	Arg	Met	Leu	Leu	Thr	Lys	Pro	Thr	His	Thr	Val			
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His	Tyr	Tyr	Trp	Arg	Lys	Phe	Asp	Asn	Ala	Phe	Met	Arg	Pro	Val	Phe			
		515					520					525						
Gly	Gly	Arg	Gly	Phe	Val	Pro	Tyr	Val	Pro	Gly	Ser	Pro	Thr	Glu	Arg			
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 <212> DNA
 <213> Ipomea nil

<223> Nucleotide sequence of promoter region of gene
encoding for protein regulating the pH of vacuoles

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